

The figure displays a sequence alignment of the protein SgK496.h across multiple entries. The x-axis represents amino acid positions, ranging from approximately 2600 to 3200. The y-axis lists the entries, each preceded by its accession number and a short description. The sequence is shown as a series of colored boxes, where each box represents a group of amino acids (e.g., hydrophobic, polar, charged) that are conserved across the different entries. The color scheme includes red, green, blue, yellow, and purple.

Accession Numbers and Descriptions:

- 83554819.q
- 10470008.q
- 15219417.p
- 15219183.p
- 15226883.p
- 83593841.q
- 15230168.p
- 15219796.p
- AK067771.q
- 15232679.p
- 83544086.q
- 83515242.q
- 15242791.p
- lias_TGFBR
- 34880204.m
- 40807349.m
- 40556610.m
- SgK496.h

Sequence Positions (X-axis):

2600 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800

2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000

3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190 3200

83554819.q ... PVTLSSTDSTANLYPVHSGMHQVQGSDYSLPASSERFYDIEQGQTSLPSVPSGYR ... YTSQCTPYSGTTSLSQFDQGSYHDSMMEGSMKEEKQPSVRVPQLKNDLDFQSYQLEMSMVPVIHDDSSNTYMSDVPVITSIQECKLSSLQPSDASKSLEYTYTAKAMSAAQDSECNEEDDRHSSG
10470008.q ... KTSR ...
15219417.p ... SSSLHYQSQIPNLAAYQLQSQVPPPSALSHYQPSITPGSSLQYQPSITPGSSYYQ ... YPQSIPGQSASSYGYIPOYYGHVQQHGGERERFPLYPDH ... SSNYSAIGETTSSI1QGHVGSQGGWAEGYYPGTSTKSTGALEAEQKV5 ... SDMK1REVEEPGVNSPKTGNBHDQNPQ ...
15219183.p ... TSFAQYQPSIPHNQAFQFQAVPPNATLQYAPSNNPSSSVHYPQSLPNSTLQ ... YPQSISSSSYQELYQYYGETEQQFP ... MQYHDHN ... SSNYSIP ... IFFPGQP ... YPHPGITQONAPVQVEENIK ... PETKVRDYVEPFRNHLATNHQNPQ ...
15226883.p ... FSTGNEPSQYPLG-QQLQFGLNHQIYTSGHMASIGYIDEKKSPALHVQGPQH ... YIPYSVNIEPLESLVHYCQPKBPEQGLREEEQIFHVQDPETPKSSEAKMRDRDSDQFQVNDHPISNLSAKEPKMRDRSSTRPVNEYVSSMPSLDLIVPVDRLDKEEPAFTVQTSSSTPFD-SSS ...
15230168.p ... FTQPMQWSESSATPSACLTQRQTMKQPSRMQSSADKSILNQBEYENKSVENGSNL ... KTMMPDHPQHQNQKNNJDTVIGVGTSTRHFIQISQVKDLAVPNEESGLS ... SHTNYDCMPITVETTFYSEKLSVTPENA ...
15219796.p ... YCN ... TNAVFHFMKMOIPRNSFGQQSPPTSPSVHVRKANTDVPYFADQ ... NGCFDFDYLAAFPQONRRFFFETTTQK-QKHPFVN-LHDRPKPSDDIY ... PHG-QAYIAEAKMNTLKRNALSDPQ ...
AK067771.q ... MNHIVVUSAPAPN ... GNSQIDP ...
15232679.p ... YVVPMTVHADPPHSFQLETVSSEKPV1GKMMQQQGQYTPPSBHPH ... QDSPLSVSSHOFPLFAAHMSMAPLNQSISSTPVLIINPMQTOEFLNGLNYHAAGKLVLPTEPRTAXQGTISPGIIPFDGYGGGSQVPPSNHVVLPDGFSFYQOVT ...
83544086.q ... FSNAAAAPFQVFNQCEIAAEPRAPPQFPEARYAQLPSQLPPLPPVFMNDREAMQCLNQAMPNGNGLREDCMNCMLKALPHASHDVFDVNDYQGSDMHHGPGPETVYVMSLR ... EDVARIMMPARAVFVHHEREMYQAQVEEIP-NTVLDIFPSGLHQNQVYVH ... HSPKXRYREVEHPSQHVNWLVPAGAVIQQN ... AGFPGNLGRG-PNFLDGSQSMYDHCRLSPFHKGQDPRVPRPQIHFQDTSMTNEYSGHPTNCSPCDNCR ... GEREFLVNLQDVRLENGVWKQ ...
152421524.q ... HSQARYGENDWPSFAYISPQHGTVHGDV ... R-DFFIISP ... RFQVQGAEDFD-E ... ERIPDFVR ... HSPKXRYREVEHPSQHVNWLVPAGAVIQQN ... AGFPGNLGRG-PNFLDGSQSMYDHCRLSPFHKGQDPRVPRPQIHFQDTSMTNEYSGHPTNCSPCDNCR ... GEREFLVNLQDVRLENGVWKQ ...
15242791.p ... SGQMLAQRYGEVEGTWSP-FYSPRHHGHD-RTFQEFPSSPSSARYRMPYGEIIPDKGLDRMPEEYVR ... PQASHHPPFYEHQAHIPDSVWWVPAQAMPPESKGQFPGNVLHGGPGCCYEGGNCGENCRCVPHRNH ... QLLEQSNIGNN-CFPVHCAHCPPNRESFLNTPDKPT-H ...
lias_TGFBR ... PCHSRHPAVDVLSDLANDFLPVITYALHKDELSERDEQELQEIIR ... KYFSPFPVFFFVVPIL ... EIIRSSSSGRADSERSPLSQGLMDLGYLSSHRNCMASDODCRAOSMLVQSEKLR ...
PCHSRHPAVDVLSDLANDFLPVITYALHKDELSERDEQELQEIIR ... KYFSPFPVFFFVVPIL ... EIIRSSSSGRADSERSPLSQGLMDLGYLSSHRNCMASDODCRAOSMLVQSEKLR ...
PCPCHRPSPVDSLSDLANDFLPVITYALHKDELSERGEQELREVR ... QYFSPFPMFFVVPKL ... EIISSSSGRAESERSPLYQLVLDLGYLSSHRNCVPSDDCRAOSMLVQSEKLR ...
PCQGLRPTVVLGDLVNDFLPVITYALHKDELSERDEQELQEIIR ... KYFSPFPVFFFVVPKLGESEIISDSTRMESERSPLYQLDILGYLSSHRNCVPSDDCRAOSMLVQSEKLR ...

3410 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600
83554819.q ... SGVAKEEIASDPAELEGKTCNL ... ARAINLNDPATVDSVTPKECANVTSQTSFSEQLIGEKRSTSMDSTMTRNVKCNLNDATDQGKJIKV ...
10470008.q ... KVEAGAHAVSRHPPR ... RNTATNMTRKNS ... QATEQVKGSPRKOL ...
15219417.p ... -IDDVEVRHNQVRERMAVATTPPSQD-AHLLPPSRDPRQNTTAKPATYRDAVITQGVPLSG ... IEDQLSSTSSSTYAPVHDSE ...
15219183.p ... -ADDTEVKN ... REPSVATTVPSCDAAHMLPPRDRTPQNTPVPKSPTYRDARVITEQVQVSG ... EDDDLSTSCTGCLVHDTSE ...
15226883.p ... TLESKSLRKSEDHEVNNLSAKEPKMRKHEHSTTRVNEYSSVSSSDSMPQDALKKEAPEIMKMSLNSTPDKSLSVYQPKSLRSLQKETGAFDNTENGMKKNQDNQFCILLGGFSVSCHGTSNNSSSVNSNQDFQVTPQHSEFERTDPTT-NEKLSSDDSALFALPIS ... ESSSETHEANMESO ...
83593841.q ... VLSAEGMTHAFSDPLLKDRTVQLAANLSLAGGSHIASFQEIYQTKELERKLSVTRPFDVCVKPTDVARTEEPRLVSNHTDQPY ... NQGIVSGTSVEPTIYYYQDLSLSNVRQGHDGSTVQQWDKPYHQENRAGLKSYCARGARMSSDELALESSVPTS ...
15230168.p ... LHDESQINNQLEAFTKCPWKILRKLNRVWATSKWED-SDDIYFNNP-EGK ... RCQELLELTKEVENPSWNIWRDNNP ... DSFDQATKK-QDGSNSNSSFSPNPFSPN ... HQPAQIITSQDQDGGSVFVSLSV ...
AK067771.q ... LQATAGID5 ... VEATR ... DB-AYTDS ... LFSNQD ... PWNAVG ...
15232679.p ... MAESFQRVNDCHMCQTSFPHMHSDFIMREGNDGSTMVYFVVSAAFYASRPDDIMRIQQTDKFTGQSQFLNHSNHOQRTDLHNANLATAQEVTFPVNEI ... ISFVDPKIGKDEIDMGTSSQQMARK ...
83544086.q ... IPNEKDRVVRSPGSANSIDSQHSSQHIMQQPLPQQQQQQLPSQGQMAQYVVKQNS ... PNNQLTGEGCSLGSQNRHEDGLTRDNVSPVAPAVENTYMAN ... VRDVMDDSLRLSPSEASASTBQPKPVMPPEN-GVPQNAIEENSQGFDTRAPRERVSQNTTFFDVSEPKVQD ...
83515242.q ... TGGHPPPMFYNESSHSHDRAWHAH-ANOSHQRYEDPRLHMPGSAARAMEPYIVDNSSVTSLSRSRSHESPYFHGSQVSDTYHINQQVGVGGPVVQTP ... GFEESTQHYS-HSSTYQADPFVQMQQNN-LPPLQSLRRRANSVHTGSPYESPILP1PINCNGFVRNTGDSVPRIPGM ...
15242791.p ... HGAYP ... NETFGPDRGMVWQQQVN-NPFRREEGRSHISNVGRPNHDYTPDYP-VSNYPLGQRAYG ... HPIISNEGFDKPLG-GIPLNSAN ... RSAEERGFHYGNLNYLPPGPDHSIHSAGHSHMHFQPNIWQNVSNPIAG ... PPGPLMQLINGTVNQT VIRNP-IETAP ...
lias_TGFBR ... QLSTFSHQLLQTRLVDAAKALNAVHSHCLDIFIN ... QAFDMQRDLQTPKRLYEYTR ... KKENELYESLMNIANRKQEEMKDMDIVETLNTMKKEELLDDAANMEFKDVIEWPENGETV ...
QLSTFSHQLLQTRLVDAAKALNAVHSHCLDIFIN ... QAFDMQRDLQTPKRLYEYTR ... KKENELYESLMNIANRKQEEMKDMDIVETLNTMKKEELLDDAANMEFKDVIEWPENGETV ...
QLSTFSHQLLQTRLVDAAKALNAVHSHCLDIFIN ... QAFDMQRDLQTPKRLYEYTR ... KKENELYESLMNIANRKQEEMKDMDIVETLNTMKKEELLDDAANMEFKDVIEWPENGETV ...
HLSLTSFHQVQLQTRLVDAAKALNLVHCHCLDIFIN ... KKENELYESLMNIANRKQEEMKDMDIVETLNTMKKEELLDDAANMEFKDVIEWPENGETV ...

3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800
83554819.q ... QQADHSASPVHFWSD ... TPNAIPITVQGCDPFVPSSTSSLDDSHKEPITPKKDNKDIVGMSERTSPDILSDFFANTAAQSLSP ... FNEPVLISLMMHNEPQWPSFRNLIAQNEFHKNEQDLAKIEBGVYPLVHABHDAVNVKNAVPQNDVHLLETYIPVSSGQINLDSILPPCF ...
10470008.q ... QFTSHDNKMKLKTYS ... TQEEAVSHSA ... SHNKTENMKR ... SDFDPTPSRCHDDTINSTNLHI ... LEKSITTNNKQKQ ... AVMCIDILKKNHPPPEPTKVR ... SERQERPNSPKPDHLSLSTARCRS-VGADR ...
15219417.p ... HHTHDKVETIEFKVQVSDETLESELPFHKIVNPDAKNDRNNVNGDTEIIGVPSLNSHVAAMSHVPIPEQASLQSDLDLIDIDNDRPDRFLSEIISQASIEDSTT-VRPVPHGDAEVMSVQHNDRKNWSYQFQLAEDQFQIQRVVDLQDADS-RIPSDRKDGESELLRYPVSLPDRGICSTNLNAPQTLQDQDYGNGFSEKD ...
15219183.p ... DVENISGNVVASNETLQD ... KRTVPSGGIETEARNLHSDTVERSHDPEQKTTQTSGG ... WLINDNDRPQDLSSEIFAKALSDMPSGANQYQHDGAGVSLNENBDPKWNSYQFDRVADYIERTP-DRGIVAYIERTP ...
15226883.p ... NVHPTAPVIFAPDSIWTIAEG ... SMSQSEKKNVEINTPEHVSQETEAKAVPQGHNEKG-DIVVDNDRFREFLADIKTESLNFPG-LGPLHADGAGVSLSNQDPTKWSYFRNLQDEFERKDLSSLMDQDHPGFTSMINT-NGVFDYDYSPPQSEKVAASSQIHPQIHFQDNIPKPDVS ...
83593841.q ... ANDHSCSPLNECSIG ... SRIENSDLGSLQDKLNQGRAAADYETACVGSNDKVKFLPINSFADAFASQISMVNRSSVYQNLQKLDQSSVHNVYGLATSLTQMSDNN-FPVCVSSREVPLERYNITRNVYVNGFDNEQMKLN-DRMHNQVMDAPVIVEDATDQALGLILSRRPLV ...
15230168.p ... TNEN-YLDCSR ... EKFNGQFQHDMSLDILIRSHSTSATDQLCSTTKSDK ... ADYSSPNTNPVVFVLR ... QEPMPRHDLETN ... SDDSDTQKSLP ... REESIYHSGPLPKRVGSRETTFMHTQGSDFFSKSLQPLQVIVEDTIVNEISDNLISATIVP ...
AK067771.q ... ASAVP ... PRLNKLNKEPAVSGD-PYVEGHGLAIN ... SSN-AATLLEEGNLP ... LIQDRTFQKDYEPPEPSQ ... KGYGEETIQLQVAEAG ...
15232679.p ... NMFLHDTSQGSPVSPNIDHTDSAKRLTRVVLQHGESQESKCVPSQPLLPGNQYSLVGGQFDSAEQSSNPAVDSTLSSSLPSSNPAIDKHESSKSLFNSQDFPNLQTNENVDK-LDNLNSKVIL ... ENDLLIGLWFSLKSGEEEEEHQKELQVNAEAG ...
83544086.q ... TEPAFSPSIASSYLNHVQHNVSHMMSIIGGPYSSYVVAATPGCPGVPSAYGVLDVXANSAVPLSERKDVHHEAPNANAQVPAALVNHAQVNDQTCR- ... SGLQGQFQGNDPWKVVNTHALP1RPKRVASENISPKDHSFNSLNLCKGPDNLPAEDVALHQSQDIDKDAHTEIGRFIKDMGTDSPDL ...
83515242.q ... AYDNLWNPWSNSGIPYTRVGHDPDPAVENSNSQGQVQYQPLPAFESVQNCQPAIMBLTQDLSRMDINPLKKLEPHEKTRNANEITB-QHAMDPSALTTHIGVVEFDPKRQKPVETEYTVTNSKVEHGGATALQECGDISERDPLFALSAKKAELDS ...
15242791.p ... RYSTGMENQGVLVGS-PORISFGDCMSSLLQGPSPYNN ... PHQDRAFLDNNWVSESPNTPVHNEILQWRPQLEPGLQDQTMQPSVTSQSLQEQGEEQVYNTQISNG ... VEYQDKPQWPLQAGKDDGMNLVNEVNSAATLEGELSVERLSLPELMESVRLSVPKRAELEGA ...
lias_TGFBR ... TREIKSCIRQIQLIELIISRLNQAVANKLISSVYDLYRESFVGTLERCLQSLKESQDLSVHITSNYLKQILNAAYHVEFTFHGSQSVTRMLWQEIKQIIQRIWTWNPPITITLEWKRKVAQEAIDSLSSAKLAKSICSQFRTRLNSSHEAFAASLR ...
34880204.m ... TREIKSCIRQIQLIELIISRLNQAVANKLISSVYDLYRESFVGTLERCLQSLKESQDLSVHITSNYLKQILNAAYHVEFTFHGSQSVTRMLWQEIKQIIQRIWTWNPPITITLEWKRKVAQEAIDSLSSAKLAKSICSQFRTRLNSSHEAFAASLR ...
40807349.m ... TREIKSCIRQIQLIELIISRLNQAVANKLISSVYDLYRESFVGTLERCLQSLKESQDLSVHITSNYLKQILNAAYHVEFTFHGSQSVTRMLWQEIKQIIQRIWTWNPPITITLEWKRKVAQEAIDSLSSAKLAKSICSQFRTRLNSSHEAFAASLR ...
40556610.m ... TREIKCIRQIQLIELIISRLNQAVANKLISSVYDLYRESFVGTLERCLQSLKESQDLSVHITSNYLKQILNAAYHVEFTFHGSQSVTRMLWQEIKQIIQRIWTWNPPITITLEWKRKVAQEAIDSLSSAKLAKSICSQFRTRLNSSHEAFAASLR ...
Sgk496.h ... TREIKCIRQIQLIELIISRLNQAVANKLISSVYDLYRESFVGTLERCLQSLKESQDLSVHITSNYLKQILNAAYHVEFTFHGSQSVTRMLWQEIKQIIQRIWTWNPPITITLEWKRKVAQEAIDSLSSAKLAKSICSQFRTRLNSSHEAFAASLR ...

83554819.q	SK-----
10470008.q	-----
15219417.p	PSAHRA SK--
15219183.p	PPAHRA SK--
15226883.p	AVNQIHK---
83593841.q	-NK-----
15230168.p	RENKP-----
15219796.p	-----
AK067771.q	PQK-----
15232679.p	STQGPQS---
83544086.q	-----
83515242.q	-----
15242791.p	-----
1ias_TGFBR	-----
34880204.m	RPSRGLDDST
40807349.m	RPSRGLDDST
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